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COPY OF PAPERS ORIGINALLY FILED PATENT

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### IN THE UNITED STATES PATENT AND TRADEMARK OFFICE

In re Application of: Mount et al.

**Examiner: Not Assigned** 

Serial No.: 09/835,976

Group Art Unit: Not Assigned

Filed: April 16, 2001

Docket No.: 1242/26/2

Confirmation No.: 3961

26/2 <del>41-</del>...

-#->/

For: PURIFIED AND ISOLATED POTASSIUM-CHLORIDE COTRANSPORTER NUCLEIC ACIDS AND POLYPEPTIDES AND THERAPEUTIC AND

SCREENING METHODS USING SAME

STATEMENT THAT SEQUENCE LISTING AND COMPUTER READABLE COPY ARE THE SAME

Commissioner for Patents Washington, D.C. 20231

Sir:

In accordance with 37 C.F.R. § 1.821(f), applicants hereby state that the Sequence Listing information recorded in computer readable form is identical to the written Sequence Listing on paper.

Although a check is being submitted, the Commissioner is hereby authorized to charge any deficiency or credit any overpayment associated with the filing of this correspondence to Deposit Account Number <u>50-0426</u>.

Respectfully submitted,

JENKINS & WILSON, P.A.

Date: 10 15 0

Bv

Arles A. Taylor, Jr.

Registration No. 39,395

Suite 1400 University Tower 3100 Tower Boulevard Durham, North Carolina 27707 Telephone: (919) 493-8000 Facsimile: (919) 419-0383

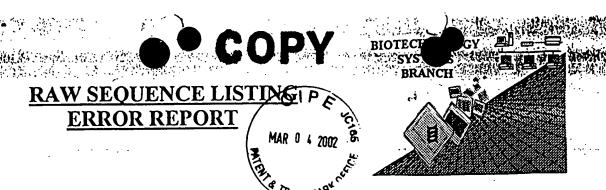
Customer No. Bar Code Label:

1242/26/2

AAT/ajm

25297

PATENT TRADEMARK OFFICE



The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 09/835,976Source: 0/PEDate Processed by STIC: 5/8/200/

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.
PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:

1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,

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FOR CRF SUBMISSION QUESTIONS, PLEASE CONTACT MARK SPENCER, 703-308-4212.

FOR SEQUENCE RULES INTERPRETATION, PLEASE CONTACT ROBERT WAX, 703-308-4216. PATENTIN 2.1 c-mail help: patin21help@uspto.gov or phone 703-306-4119 (R. Wax) PATENTIN 3.0 c-mail help: patin3help@uspto.gov or phone 703-306-4119 (R. Wax)

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE <u>CHECKER</u> <u>VERSION 3.0 PROGRAM</u>, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW:

## Checker Version 3.0

The Checker Version 3.0 application is a state-of the-art Windows based software program employing a logical and intuitive user-interface to check whether a sequence listing is in compliance with format and content rules. Checker Version 3.0 works for sequence listings generated for the original version of 37 CFR §§1.821 – 1.825 effective October 1, 1990 (old rules) and the revised version (new rules) effective July 1, 1998 as well as World Intellectual Property Organization (WIPO) Standard ST.25.

Checker Version 3.0 replaces the previous DOS-based version of Checker, and is Y2K-compliant. Checker allows public users to check sequence listings in Computer Readable form (CRF) before submitting them to the United States Patent and Trademark Office (USPTO). Use of Checker prior to filing the sequence listing is expected to result in fewer errored sequence listings, thus saving time and money.

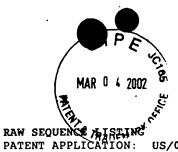
Checker Version 3.0 can be down loaded from the USPTO website at the following address:

http://www.uspto.gov/web/offices/pac/checker

## ERROR DETECTION SUGGESTED CORRECTION

SERIAL NUMBER: <u>09/835,97</u>6

		The number/text at the end of each line "wrapped" down to the next line.
1	Wrapped Nucleics	This may occur if your file was retrieved in a word processor after creating it.
		Please adjust your right margin to .3, as this will prevent "wrapping".
2	Wrapped Aminos	The amino acid number/text at the end of each line "wrapped" down to the next line.
	•	This may occur if your file was retrieved in a word processor after creating it.
		Please adjust your right margin to .3, as this will prevent "wrapping".
3	Incorrect Line Length	The rules require that a line not exceed 72 characters in length. This includes spaces.
4	Misaligned Amino Acid	The numbering under each 5th amino acid is misaligned. This may be caused by the use of tabs
	Numbering	between the numbering. It is recommended to delete any tabs and use spacing between the numbers.
5	Non-ASCII	This file was not saved in ASCII (DOS) text, as required by the Sequence Rules.
		Please ensure your subsequent submission is saved in ASCII text so that it can be processed.
6	Variable Length	Sequence(s) contain n's or Xaa's which represented more than one residue.
		As per the rules, each n or Xaa can only represent a single residue.
		Please present the maximum number of each residue having variable length and
		Indicate in the (ix) feature section that some may be missing.
7	Patentin ver. 2.0 "bug"	A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid
		sequence(s) Normally, Patentln would automatically generate this section from the
		previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. This applies primarily to the mandatory <220>-<223>
		sections for Artificial or Unknown sequences.
8	Skipped Sequences	Sequence(s) missing. If intentional, please use the following format for each skipped sequence:
	(OLD RULES)	(2) INFORMATION FOR SEQ ID NO:X:
		(i) SEQUENCE CHARACTERISTICS:(Do not insert any headings under "SEQUENCE CHARACTERISTICS")
		(xi) SEQUENCE DESCRIPTION:SEQ ID NO:X:
		This sequence is intentionally skipped
		Please also adjust the "(iii) NUMBER OF SEQUENCES:" response to include the skipped sequence(s).
9	Skipped Sequences	Sequence(s) missing. If intentional, please use the following format for each skipped sequence.
	(NEW RULES)	<210> sequence id number
\		<400> sequence id number 000
10	Use of n's or Xaa's	Use of n's and/or Xaa's have been detected in the Sequence Listing.
··· <u> </u>	(NEW RULES)	Use of <220> to <223> is MANDATORY if n's or Xaa's are present.
	(NEW NOLLS)	In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.
11	Use of "Artificial"	Use of "Artificial" only as "<213> Organism" response is incomplete, per 1.823(b) of New Sequence Rules.
	(NEW RULES)	Valid response is Artificial Sequence.
12	Use of <220>Feature	Sequence(s) are missing the <220>Feature and associated headings.
	(NEW RULES)	Use of <220> to <223> is MANDATORY if <213>ORGANISM is "Artificial Sequence" or "Unknown"
		Please explain source of genetic material in <220> to <223> section.
		(See "Federal Register," 6/01/98, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of new Rules)
13	Patentin ver. 2.0 "bug"	Please do not use "Copy to Disk" function of Patentin version 2.0. This causes a corrupted
		file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing).
		Instead, please use "File Manager" or any other means to copy file to floppy disk.
		AMC - Biotechnology Systems Branch - 4/06/2001





OIPE

W SEQUENCE AISTING DATE: 05/08/2001 TENT APPLICATION: US/09/835,976 TIME: 15:55:17

Input Set : A:\PTO.txt

Output Set: N:\CRF3\05082001\1835976.raw

Does Not Comply Corrected Diskette Needed

Apr 4

3 <110> APPLICANT: Mount, David B.
4 Delpire, Eric
5 Gamba, Gerardo

6 Alfred L. George, Jr.

8 <120> TITLE OF INVENTION: PURIFIED AND ISOLATED POTASSIUM-CHLORIDE COTRANSPORTER NUCLEIC ACIDS

AND

9 POLYPEPTIDES AND

4644 <210> SEQ ID NO: 16

10 THERAPEUTIC AND SCREENING METHODS USING SAME

12 <130> FILE REFERENCE: Attorney Docket No. 1242-26-2

> 14 <140> CURRENT APPLICATION NUMBER: US/09/835,976

15 <141> CURRENT FILING DATE: 2001-04-16

17 <160> NUMBER OF SEQ ID NOS: 131

19 <170> SOFTWARE: PatentIn Ver. 2.1

#### ERRORED SEQUENCES

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RAW SEQUENCE LISTING DATE: 05/08/2001 PATENT APPLICATION: US/09/835,976 TIME: 15:55:17

Input Set : A:\PTO.txt

Output Set: N:\CRF3\05082001\I835976.raw

4908 ttgaaatgtg ttattttca agttatcttt tgtattgcag tcaaaagtag ctagcgtaag 660

4910 aggaagattt tgcgaggttc cccccacttt ttttgttctt aaaaagaaca aa

4833 Ser Phe Phe Pro Ser Asn Val Glu Gln Phe Ser Glu Gly Asn Ile Asp 4834 900 4836 Val Trp Trp Ile Val His Asp Gly Gly Met Leu Met Leu Leu Pro Phe 915 920 925 4839 Leu Leu Lys Gln His Lys Val Trp Arg Lys Cys Ser Ile Arg Ile Phe 935 4842 Thr Val Ala Gln Leu Glu Asp Asn Ser Ile Gln Met Lys Lys Asp Leu 955 4843 945 950 4845 Ala Thr Phe Leu Tyr His Leu Arg Ile Glu Ala Glu Val Glu Val Val 970 965 4848 Glu Met His Asp Ser Asp Ile Ser Ala Tyr Thr Tyr Glu Arg Thr Leu 980 When numbering the first amend acid on a line, begin the number directly under the first letter of the amend acid. 4851 Met Met Glu Gln Arg Ser Gln Met Leu Arg His Met Arg Leu Ser Lys 995 1000 1005 4854 Thr Glu Arg Asp Arg Glu Ala Gln Leu Val Lys Asp Arg Asn Ser Met 1020 1010 1015 4857 Leu Arg Leu Thr Ser Ile Gly Ser Asp Glu Asp Glu Glu Thr Glu Thr E--> 4858 025 ) 1025 1030 1035 1040 4860 TYP Gln Glu Lys Val His Met Thr Trp Thr Lys Asp Lys Trr Met Ala 1050 1055 1045 4863 Ser Arg Gly Gln Lys Ala Lys Ser Met Glu Gly Phe Gln Asp Leu Leu 1060 1065 1070 4866 Asn Met Arg Pro Asp Gln Ser Asn Val Arg Arg Met His Thr Ala Val 4867 1075 1080 1085 4869 Lys Leu Asn Glu Val Ile Val Asn Lys Ser His Glu Ala Lys Leu Val 4870 1090 1095 1100 4872 Leu Leu Asn Met Pro Gly Pro Pro Arg Asn Pro Glu Gly Asp Glu Asn E--> 4873(105) 1105 1115 1110 4875 Tyr Met Glu Phe Leu Glu Val Leu Thr Glu Gly Leu Glu Arg Val Leu 1125 1130 4878 Leu Val Arg Gly Gly Gly Ser Glu Val Ile Thr Ile Tyr Ser 1145 1140 4882 <210> SEQ ID NO: 17 4883 <211> LENGTH: 712 4884 <212> TYPE: DNA 4885 <213> ORGANISM: Homo sapiens 4887 <400> SEQUENCE: 17 see den 10 on Eva Summany Sheet 4888 agacaggaat coggttotgo cootgoatoo toototgott caccottotg toagtagtgt 60 E--> 4890 gggttatttt ttdnbgttat gcatgtgcac ctttcccacc agacccaagt ggattgtcga 120 4892 catcaaaaag accgggtggc tttgcataca cctcccccca gccagacctg tggggtattc 180 E--> 4894 acctgata(n) caacaggtgg ccgggtgtac accttttagc aatctgatcc acgctatagt 240 4896 cgcctgataa aggtttgcct gcacgcactt ggcccaacta gaacccgtgg gacactcacc 300 4898 agataaagga cttacctcga caggaaactg ggggctgagg ggagggaggc ttcatctgct 360 4900 gccctgagac catggcactg agccttcagc cccggaccag aggggttagc taggtagctc 420 4902 ttcattctga aggaaagaag tcacacaaga ttggcattgt tttgtctttt tgtttttgt 480 4904 ttttttctct cttaaaaaat atattcacct attggtgatg cactttctag gacagtcggc 540 4906 ttgaattctg agtagaagta ttcttagttg gggctttgtg tgtggtgtga atcaaggtta 600





RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/835,976

DATE: 05/08/2001 TIME: 15:55:18

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Output Set: N:\CRF3\05082001\I835976.raw

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     4914 <211> LENGTH: 1014
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     4916 <213> ORGANISM: mouse
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     4923 cgttatgcat gcgcatctct cccaccagac ccaagtggat tatcgacctc aaaaacatcg 180
     4925 qqtqqctcaq cacacacctc ctcccaqcca gacctgtggg gtattcacct gatacacaac 240
     4927 aggtggctgg tgcacacctt tgcgcaatct gatccacgct cttatacgcc tgataagggt 300
     4929 gggcctgcat gctccgtcct cagctagaac cgtgggacac tcggcagata aaggactaac 360
     4931 tacctcatcc ggaccctggg ggttgagcag agggaggcgt caccagctgc tgtgagatca 420
     4933 tggcacggag cccacagccc tggaccaggg gagatagcta ggattctgaa agaaccaagt 480
E--> 4935 tatacaggat tagcatcgtt ttgttcttat tttgttttct cgaanattat ttttcagtta 540
     4937 ctggtggggc actttataaa acagctggct tgaattctat acacggattc ttaattgggc 600
     4939 ctttgtgggc tgtaaatcag ggtaattgag ggtttttggt tttttttccc cttctatttt 660
     4941 tgcaatcaga agtagctagt gtaggaggaa gagtttttgt gagcttttcc ttttttcttt 720
     4943 gtcaaaaagg aaagggggg gaaaatgcat ccaccagaag ccaccaccaa gatgtcctca 780
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     4947 ccggacctca gctctcggtc tagttctcga gtaagattta gctcccgaga aagtgtgcca 900
     4949 gaaacaagee qtagtgagee tatgagegaa etgtetgggg ctactactte tetggeaact 960
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     4962 catatgettt gaacttaage aacaatggaa accgteettt tgttttetga gttgacatag 120
     4964 tgccagtctt cattaaagag ggtagtttgt gaaataaagt gttccctgat ctttctcgtg 180
     4966 tgaagtaaaa ggacagatga tgagtaaggt tgagatgatg gaacccagag aagtggcaat 240
     4968 aaattaaagg aaacaagtgg gagacacagg gtggacagct cttgatgagc tcacgggctt 300
     4970 tagetttetg cegeetggag aaactgeeca gacagttgga gttetacagg ttaataacaa 360
     4972 taagctgggg tggagtgctt aagcctttta agagaatgat aaacagggcg gaaggcgtgt 420
     4974 cttcaagcgt cccactccct tggggctatg gtcacgtggg ctcagtactt cccgattccc 480
     4976 agccactgtc tecetagget gtgetetgag tgtqqaqgga gagaggeagg gaegeaeggg 540
E--> 4978 aaggaaattt aaacgctgaa agcaagggtc tgthigtaag aacaatgccg cacttcactg 600
     4980 tgaccaaggt agaagaccca gaggaggggg cagctggccc ceteteteet gagcccaget 660
     4982 cagcagaagt aaaagcccgg attcaggatc cccaagaacc aggtaagtcc tgcgcttgta 720
     4984 gcgtcggggg acccacagac tagt
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                                             next page
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     5326 <400> SEQUENCE: 46
     5327 gtgggggcag agaaacatgg aggaggagca cacctggggt gttcgtaatg atgaggactg 60
     5329 cagagactga tgctggcctc cctggcaggc cccacgcatg ggcaccttca tgggcgtgta 120
     5331 cctqccqtqc ctqcaqaaca tctttqqcqt catcctcttc ctqcqqctca cctqqqtqgt 180
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5333 gggcattgca ggcatcatgg agtccttctg catggtgttc atctgctgct cctgtgtgag 240





RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/835,976

DATE: 05/08/2001 TIME: 15:55:18

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Output Set: N:\CRF3\05082001\1835976.raw

E--> 5335 tgacacccct cccctcacca cccctgaca gctggggctt ggcagaggcc tggngggtgg 300 ) tem / O 6892 <210> SEQ ID NO: 113 6893 <211> LENGTH: 361 P. 7 ( rest page) 6894 <212> TYPE: PRT 6895 <213> ORGANISM: Xenopus laevis 6897 <400> SEQUENCE: 113 6898 Arg His Glu Gly Thr Val Leu Leu Gly Asp Tyr Leu Asp Ser His Ala 10 6901 Glu Ser Gln Ala Ala Glu Gln Ala Leu Lys His Leu Met Glu Gln Glu 6902 20 25 30 6904 Lys Val Lys Gly Phe Cys Gln Val Val Ala Gln Lys Leu Lys Glu 40 6905 35 6907 Gly Leu Ser His Leu Ile Gln Ser Cys Gly Leu Gly Gly Met Arg His 6908 50 55 60 6910 Asn Thr Val Ile Met Ser Trp Pro Ser Ser Trp Arg Gln Ser Asp Asp 6911 65 70 75 6913 Ser Arg Ala Trp Lys Ser Phe Ile Thr Thr Ile Arg Val Thr Thr Ala 85 90 6914 6916 Ala Arg Gln Ala Leu Leu Val Ala Lys Asn Val Ser Phe Phe Pro Gly 6917 105 100 6919 Ser Arg Glu Thr Leu Ala Glu Gly His Ile Asp Val Trp Trp Ile Val 120 125 6920 115 6922 His Asp Gly Gly Met Leu Met Leu Pro Phe Leu Leu Lys Gln His 140 130 135 6925 Lys Val Trp Arg Lys Cys Lys Met Arg Ile Phe Thr Val Ala Gln Met 155 6926 145 150 6928 Glu Asp Asn Ser Ile Gln Met Lys Lys Asp Leu Ala Thr Phe Leu Tyr 170 165 6931 His Leu Arg Ile Ala Ala Asp Val Glu Val Val Glu Met His Asp Ser 180 185 190 6934 Asp Ile Ser Ala Tyr Thr Tyr Glu Arg Thr Leu Met Met Glu Gln Arg 6935 195 200 205 6937 Ser Gln Met Leu Arg Gln Met Arg Leu Ser Lys Thr Asp Arg Glu Arg 6938 210 215 6940 Glu Ala Gln Leu Val Lys Asp Arg Asn Ser Ile Leu Arg Leu Thr Ser 230 235 6943 Val Gly Ser Asp Asp Glu Asp Thr Glu Ala Ala Pro Glu Arg Val 250 245 6946 His Met Thr Trp Thr Arg Asp Lys His His Ala Val Arg Val Ala Gln 6947 260 265 6949 Ser Lys Pro Met Pro Ser Cys Gln Asp Leu Leu Asn Ile Arg Pro Asp 275 280 6952 Gln Ser Asn Val Arg Arg Met His Thr Ala Val Lys Leu Asn Glu Val 290 295 300 6955 Ile Val Asn Lys Ser His Asp Ala Lys Leu Val Leu Leu Asn Met Pro 315 310 6958 Gly Pro Pro Arg Asn Pro Gln Gly Asp Glu Asn Tyr Met Glu Phe Leu 325





RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/835,976

DATE: 05/08/2001 TIME: 15:55:18

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 $E\rightarrow$  6961 Glu Val Leu Thr Glu Gly Leu Glu Arg Val Leu Val Val Arg Gly Gly

962 340 345 3

6964 Gly Thr Glu Val Ile Thr Ile Tyr Ser

E--> 6965 355 360

FYI

Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.





DATE: 05/08/2001

TIME: 15:55:19

# VERIFICATION SUMMARY

PATENT APPLICATION: US/09/835,976

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Output Set: N:\CRF3\05082001\I835976.raw

L:14 M:270 C: Current Application Number differs, Replaced Application Number L:15 M:271 C: Current Filing Date differs, Replaced Current Filing Date L:59 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:1 L:60 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:1 L:67 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:1 L:68 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:1 L:303 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:1 L:304 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:1 L:417 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:2 L:423 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:2 L:600 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:2 L:650 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3 L:651 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3 L:762 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3 L:763 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3 L:910 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3 L:911 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3 L:981 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:4 L:1062 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:4 L:1176 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:4 L:1239 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:5 L:1240 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:5 L:1371 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:5 L:1372 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:5 L:1491 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:5 L:1492 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:5 L:1630 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:6 L:1729 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:6 L:1819 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:6 L:1858 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:7 L:1859 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:7 L:1926 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:7 L:1927 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:7 L:2062 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:7 L:2063 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:7 L:2510 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:9 L:2511 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:9 L:2630 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:9 L:2631 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:9 L:2738 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:9 L:2739 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:9 L:2895 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:10 L:2982 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:10 L:3063 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:10 L:3143 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:11 L:3144 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:11 L:3203 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:11 L:3204 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:11





DATE: 05/08/2001

TIME: 15:55:19

#### VERIFICATION SUMMARY

PATENT APPLICATION: US/09/835,976

Input Set : A:\PTO.txt

Output Set: N:\CRF3\05082001\1835976.raw

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L:3569 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:12
L:4858 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:16
M:332 Repeated in SeqNo=16
L:4890 M:340 E: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:17
M:340 Repeated in SeqNo=17
L:4935 M:340 E: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:18
L:4978 M:340 E: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:19
L:5335 M:340 E: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:46
L:6680 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:111
L:6808 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:112

L:6961 M:333 E: Wrong sequence grouping, Amino acids not in groups! L:6961 M:320 E: (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS:1

L:6965 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:113

L:6965 M:252 E: No. of Seq. differs, <211>LENGTH:Input:361 Found:362 SEQ:113

L:7159 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:131





RAW SEQUENCE LISTING DATE: 05/08/2001 PATENT APPLICATION: US/09/835,976 TIME: 15:55:17

Input Set : A:\PTO.txt

Output Set: N:\CRF3\05082001\I835976.raw

4692 Lys Val Ser Ser Leu Leu Asn Arg Met Ala Asn 4693 145						
4690 130 4692 Lys Val Ser Ser Leu Leu Asn Arg Met Ala Asn 4693 145 4695 Gln Gly Ala Lys Glu His Glu Glu Ala Glu Asn 170 4698 Lys Lys Pro Thr Lys Thr Pro Gln Met Gly Thr 180 4701 Leu Pro Cys Leu Gln Asn Ile Phe Gly Val Ile 4702 200 4704 Thr Trp Val Val Gly Thr Ala Gly Val Leu Gln 4705 210 4707 Leu Ile Cys Cys Cys Cys Thr Met Leu Thr Ala 4708 225 4710 Ile Ala Thr Asn Gly Val Val Pro Ala Gly Gly 325 4710 Ile Ala Thr Asn Gly Pro Glu Phe Gly Gly Ala 171 4711 245 4713 Ser Arg Ala Leu Gly Pro Glu Phe Gly Gly Ala 171 4714 260 4716 Tyr Leu Gly Thr Thr Phe Ala Ala Ala Met Tyr 275 4719 Glu Ile Phe Leu Val Tyr Ile Val Pro Arg Ala 273 4720 290 4722 Asp Asp Ala Leu Lys Glu Ser Ala Ala Met Leu 315 4725 Tyr Gly Thr Ala Phe Leu Val Leu Met Val Leu 325 4726 Val Arg Tyr Val Asn Lys Phe Ala Ser Xaa Phe 1722 4731 Val Ser Ile Leu Ala Ile Tyr Ala Gly Ala Ile 1732 4732 355 4734 Pro Pro His Phe Pro Val Cys Met Leu Gly Asn 1735 4737 Arg His Ile Asp Val Cys Ser Lys Thr Lys Glu 1733 385 4738 Asn Ala Thr Cys Asp Glu Tyr Phe Val His Asn 1744 4740 4750 4740 Val Pro Ser Lys Leu Trp Gly Phe Phe Cys Asn 345 4741 420 4746 Gln Gly Ile Pro Gly Leu Ala Ser Gly Ile Ile 1747 4749 Ser Asn Tyr Leu Pro Lys Gly Glu Ile Ile Glu 1747 4749 Ser Asn Tyr Leu Pro Lys Gly Glu Ile Ile Glu 17450 4750 450 4752 Ser Ser Asp Val Leu Gly Ser Leu Asn His Glu 175	Glu	Glu (	Gly 125		Glu	Tyr
4692 Lys Val Ser Ser Leu Leu Asn Arg Met Ala Asn 4693 145 4695 Gln Gly Ala Lys Glu His Glu Glu Ala Glu Asn 1696 4698 Lys Lys Pro Thr Lys Thr Pro Gln Met Gly Thr 180 4701 Leu Pro Cys Leu Gln Asn Ile Phe Gly Val Ile 200 4704 Thr Trp Val Val Gly Thr Ala Gly Val Leu Gln 4705 4707 Leu Ile Cys Cys Cys Cys Thr Met Leu Thr Ala 235 4710 Ile Ala Thr Asn Gly Val Val Pro Ala Gly Gly 34711 4711 245 4713 Ser Arg Ala Leu Gly Pro Glu Phe Gly Gly Ala 34714 4714 260 4716 Tyr Leu Gly Thr Thr Phe Ala Ala Ala Met Tyr 275 4719 Glu Ile Phe Leu Val Tyr Ile Val Pro Arg Ala 2472 4720 290 4722 Asp Asp Ala Leu Lys Glu Ser Ala Ala Met Leu 4723 305 4728 Val Arg Tyr Val Asn Lys Phe Ala Ser Xaa Phe 3473	Met 140		_	Thr	Arg	Pro
4695 Gln Gly Ala Lys Glu His Glu Glu Ala Glu Asn 4696 4698 Lys Lys Pro Thr Lys Thr Pro Gln Met Gly Thr 4699 4701 Leu Pro Cys Leu Gln Asn Ile Phe Gly Val Ile 4702 195 4704 Thr Trp Val Val Gly Thr Ala Gly Val Leu Gln 4705 210 4707 Leu Ile Cys Cys Cys Cys Thr Met Leu Thr Ala 4708 225 4710 Ile Ala Thr Asn Gly Val Val Pro Ala Gly Gly 4711 245 4713 Ser Arg Ala Leu Gly Pro Glu Phe Gly Gly Ala 4714 4716 Tyr Leu Gly Thr Thr Phe Ala Ala Ala Met Tyr 4717 275 4719 Glu Ile Phe Leu Val Tyr Ile Val Pro Arg Ala 4720 290 4722 Asp Asp Ala Leu Lys Glu Ser Ala Ala Met Leu 4723 305 4725 Tyr Gly Thr Ala Phe Leu Val Leu Met Val Leu 4726 4728 Val Arg Tyr Val Asn Lys Phe Ala Ser Xaa Phe 4729 4731 Val Ser Ile Leu Ala Ile Tyr Ala Gly Ala Ile 4732 4734 Pro Pro His Phe Pro Val Cys Met Leu Gly Asn 4735 370 4737 Arg His Ile Asp Val Cys Ser Lys Thr Lys Glu 4743 Asn Ala Thr Cys Asp Glu Tyr Phe Val His Asn 4744 4750 476 Gln Gly Ile Pro Gly Leu Ala Ser Gly Ile Ile 476 Gln Gly Ile Pro Gly Leu Ala Ser Gly Ile Ile 476 Gln Gly Ile Pro Gly Leu Ala Ser Gly Ile Ile 476 Gln Gly Ile Pro Gly Leu Ala Ser Leu Asn His Glu 4750 4750 450 4752 Ser Ser Asp Val Leu Gly Ser Leu Asn His Glu	Tyr	Asn '		Asn	Leu	
4696       Lys Lys Pro Thr Lys Thr Pro Gln Met Gly Thr 180       185         4701       Leu Pro Cys Leu Gln Asn Ile Phe Gly Val Ile 4702       195         4704       Thr Trp Val Val Gly Thr Ala Gly Val Leu Gln 4705       210         4707       Leu Ile Cys Cys Cys Cys Cys Thr Met Leu Thr Ala 4708 225       230         4710       Ile Ala Thr Asn Gly Val Val Pro Ala Gly Gly A11       245         4711       245       230         4712       Eu Gly Thr Thr Phe Ala Ala Ala Met Tyr 250         4713       Ser Arg Ala Leu Gly Pro Glu Phe Gly Gly Ala 260         4716       Tyr Leu Gly Thr Thr Phe Ala Ala Ala Met Tyr 275         4719       Glu Ile Phe Leu Val Tyr Ile Val Pro Arg Ala 260         4720       290         4721       290         4722       Asp Asp Ala Leu Lys Glu Ser Ala Ala Met Leu 272         4723       305         4725       Tyr Gly Thr Ala Phe Leu Val Leu Met Val Leu 315         4726       325         4731       Val Ser Ile Leu Ala Ile Tyr Ala Gly Ala Ile 347         4732       355         4733       Yar Val Asn Lys Phe Ala Ser Xaa Phe 347         4731       Val Ser Ile Leu Ala Ile Tyr Ala Gly Ala Ile 347         4732       355         4734       Pro Pro His Phe Pro Val Cys Ser Lys Thr Lys Glu 3						160
4698 Lys Lys Pro Thr Lys Thr Pro Gln Met Gly Thr 4699 4701 Leu Pro Cys Leu Gln Asn Ile Phe Gly Val Ile 4702 195 200 4704 Thr Trp Val Val Gly Thr Ala Gly Val Leu Gln 4705 210 215 4707 Leu Ile Cys Cys Cys Cys Thr Met Leu Thr Ala 4708 225 4710 Ile Ala Thr Asn Gly Val Val Pro Ala Gly Gly Gly 4711 245 250 4713 Ser Arg Ala Leu Gly Pro Glu Phe Gly Gly Ala 4714 260 4716 Tyr Leu Gly Thr Thr Phe Ala Ala Ala Met Tyr 4717 275 4719 Glu Ile Phe Leu Val Tyr Ile Val Pro Arg Ala 4720 290 4722 Asp Asp Ala Leu Lys Glu Ser Ala Ala Met Leu 4723 305 4725 Tyr Gly Thr Ala Phe Leu Val Pro Arg Ala 4726 325 4728 Val Arg Tyr Val Asn Lys Phe Ala Ser Xaa Phe 4732 4731 Val Ser Ile Leu Ala Ile Tyr Ala Gly Ala Ile 4732 355 4734 Pro Pro His Phe Pro Val Cys Met Leu Gly Asn 4735 370 4737 Arg His Ile Asp Val Cys Ser Lys Thr Lys Glu 4738 385 4740 Val Pro Ser Lys Leu Trp Gly Phe Phe Cys Asn 4741 405 4743 Asn Ala Thr Cys Asp Glu Tyr Phe Val His Asn 4744 4750 476 Gln Gly Ile Pro Gly Leu Ala Ser Gly Ile Ile 4764 4774 Ass 4775 4779 Ser Asn Tyr Leu Pro Lys Gly Glu Ile Ile Glu 4765 4779 Ser Ser Asp Val Leu Gly Ser Leu Asn His Glu 4750 4750 450 4752 Ser Ser Asp Val Leu Gly Ser Leu Asn His Glu	Ile	Asn :	Thr	Glu		
4699 4701 Leu Pro Cys Leu Gln Asn Ile Phe Gly Val Ile 4702 195 200 4704 Thr Trp Val Val Gly Thr Ala Gly Val Leu Gln 4705 210 4707 Leu Ile Cys Cys Cys Cys Thr Met Leu Thr Ala 4708 225 230 235 4710 Ile Ala Thr Asn Gly Val Val Pro Ala Gly Gly 4711 245 250 4713 Ser Arg Ala Leu Gly Pro Glu Phe Gly Gly Ala 4714 260 265 4719 Glu Ile Phe Leu Val Tyr Ile Val Pro Arg Ala 4720 290 4722 Asp Asp Ala Leu Lys Glu Ser Ala Ala Met Tyr 4723 305 310 315 4725 Tyr Gly Thr Ala Phe Leu Val Leu Met Val Leu 4726 325 4731 Val Ser Ile Leu Ala Ile Tyr Ala Gly Ala 4729 340 340 4731 Val Ser Ile Leu Ala Ile Tyr Ala Gly Ala Ile 4732 355 4734 Pro Pro His Phe Pro Val Cys Met Leu Gly Asn 4735 370 4737 Arg His Ile Asp Val Cys Ser Lys Thr Lys Glu 4738 385 390 395 4740 Val Pro Ser Lys Leu Trp Gly Phe Phe Cys Asn 4741 405 4743 Asn Ala Thr Cys Asp Glu Tyr Phe Val His Asn 4744 420 4746 Gln Gly Ile Pro Gly Leu Ala Ser Gly Ile Ile 4747 435 4749 Ser Asn Tyr Leu Pro Lys Gly Glu Ile Ile Glu 4750 450 4752 Ser Ser Asp Val Leu Gly Ser Leu Asn His Glu					175	
4701 Leu Pro Cys Leu Gln Asn Ile Phe Gly Val Ile 4702	Phe	Thr	Met	Gly	Val	Tyr
4702				190		
4702	Leu	Ile 1	Phe	Leu	Arg	Leu
4705			205			
4705	Ala	Gln A	Phe	Ala	Ile	Val
4708 225 4710 Ile Ala Thr Asn Gly Val Val Pro Ala Gly Gly 4711 245 4713 Ser Arg Ala Leu Gly Pro Glu Phe Gly Gly Ala 714 260 4716 Tyr Leu Gly Thr Thr Phe Ala Ala Ala Met Tyr 275 4719 Glu Ile Phe Leu Val Tyr Ile Val Pro Arg Ala 717 275 4722 Asp Asp Ala Leu Lys Glu Ser Ala Ala Met Leu 717 4723 305 4725 Tyr Gly Thr Ala Phe Leu Val Leu Met Val Leu 717 4726 4731 Val Ser Ile Leu Ala Ile Tyr Ala Gly Ala Ile 717 4732 355 4734 Pro Pro His Phe Pro Val Cys Met Leu Gly Asn 737 4737 Arg His Ile Asp Val Cys Ser Lys Thr Lys Glu 7473 4740 Val Pro Ser Lys Leu Trp Gly Phe Phe Cys Asn 374 4740 Val Pro Ser Lys Leu Trp Gly Phe Phe Cys Asn 374 4744 420 4750 450 4752 Ser Ser Asn Tyr Leu Pro Lys Gly Glu Ile Ile Glu 14750 4752 Ser Ser Asp Val Leu Gly Ser Leu Asn His Glu 750 4752 Ser Ser Asp Val Leu Gly Ser Leu Asn His Glu 750	220	:				
4710 Ile Ala Thr Asn Gly Val Val Pro Ala Gly Gly 4711  245  4713 Ser Arg Ala Leu Gly Pro Glu Phe Gly Gly Ala 260  4716 Tyr Leu Gly Thr Thr Phe Ala Ala Ala Met Tyr 275  4719 Glu Ile Phe Leu Val Tyr Ile Val Pro Arg Ala 4720  290  4722 Asp Asp Ala Leu Lys Glu Ser Ala Ala Met Leu 4723 305  4725 Tyr Gly Thr Ala Phe Leu Val Leu Met Val Leu 4726  325  4718 Val Arg Tyr Val Asn Lys Phe Ala Ser Xaa Phe 14729  4731 Val Ser Ile Leu Ala Ile Tyr Ala Gly Ala Ile 14732  4734 Pro Pro His Phe Pro Val Cys Met Leu Gly Asn 2735  4737 Arg His Ile Asp Val Cys Ser Lys Thr Lys Glu 14738 385  4740 Val Pro Ser Lys Leu Trp Gly Phe Phe Cys Asn 395  4740 Val Pro Ser Lys Leu Trp Gly Phe Phe Cys Asn 395  4746 Gln Gly Ile Pro Gly Leu Ala Ser Gly Ile Ile 14747  435  4749 Ser Asn Tyr Leu Pro Lys Gly Glu Ile Ile Glu 14750  450  4752 Ser Ser Asp Val Leu Gly Ser Leu Asn His Glu 15	Ile	Ala 1	Ser	Met	Ser	Ala
4711						240
4713 Ser Arg Ala Leu Gly Pro Glu Phe Gly Gly Ala 260 265 4716 Tyr Leu Gly Thr Thr Phe Ala Ala Ala Met Tyr 275 280 4719 Glu Ile Phe Leu Val Tyr Ile Val Pro Arg Ala 4720 290 295 4722 Asp Asp Ala Leu Lys Glu Ser Ala Ala Met Leu 4723 305 310 315 4725 Tyr Gly Thr Ala Phe Leu Val Leu Met Val Leu 4726 325 339 4728 Val Arg Tyr Val Asn Lys Phe Ala Ser Xaa Phe 14729 340 345 4731 Val Ser Ile Leu Ala Ile Tyr Ala Gly Ala Ile 4732 355 360 4734 Pro Pro His Phe Pro Val Cys Met Leu Gly Asn 4735 370 4737 Arg His Ile Asp Val Cys Ser Lys Thr Lys Glu 4738 385 390 395 4740 Val Pro Ser Lys Leu Trp Gly Phe Phe Cys Asn 4741 405 420 425 4746 Gln Gly Ile Pro Gly Leu Ala Ser Gly Ile Ile 614 4747 435 450 450 455 4750 450 450 455 4752 Ser Ser Asp Val Leu Gly Ser Leu Asn His Glu 614 55 4752 Ser Ser Asp Val Leu Gly Ser Leu Asn His Glu 614 55 4752 Ser Ser Asp Val Leu Gly Ser Leu Asn His Glu 614 55 4752 Ser Ser Asp Val Leu Gly Ser Leu Asn His Glu 614 55 5	Ser	Sly S	Tyr	Phe	Mét	Ile
4714					255	
4716 Tyr Leu Gly Thr Thr Phe Ala Ala Ala Met Tyr 4717 275 280  4719 Glu Ile Phe Leu Val Tyr Ile Val Pro Arg Ala 4720 290 295  4722 Asp Asp Ala Leu Lys Glu Ser Ala Ala Met Leu 4723 305 310 315  4725 Tyr Gly Thr Ala Phe Leu Val Leu Met Val Leu 4726 325 339  4728 Val Arg Tyr Val Asn Lys Phe Ala Ser Xaa Phe 174729 340 345  4731 Val Ser Ile Leu Ala Ile Tyr Ala Gly Ala Ile 4732 355 360  4734 Pro Pro His Phe Pro Val Cys Met Leu Gly Asn 4735 370 375  4737 Arg His Ile Asp Val Cys Ser Lys Thr Lys Glu 4738 385 390 395  4740 Val Pro Ser Lys Leu Trp Gly Phe Phe Cys Asn 4741 405 405 410  4743 Asn Ala Thr Cys Asp Glu Tyr Phe Val His Asn 4744 420 425  4746 Gln Gly Ile Pro Gly Leu Ala Ser Gly Ile Ile 614 4747 435 450 450 455 455 4752 Ser Ser Asp Val Leu Gly Ser Leu Asn His Glu 5455 4752 Ser Ser Asp Val Leu Gly Ser Leu Asn His Glu 5455 4752 Ser Ser Asp Val Leu Gly Ser Leu Asn His Glu 5455	Val	Ala N	Gly	Leu	Cys	Phe
4717				270		
4717	Ile	[yr ]	Leu	Gly	Ala	Ile
4720 290 295 4722 Asp Asp Ala Leu Lys Glu Ser Ala Ala Met Leu Ara 305 310 315 4725 Tyr Gly Thr Ala Phe Leu Val Leu Met Val Leu Ara 325 339 4728 Val Arg Tyr Val Asn Lys Phe Ala Ser Xaa Phe Ara 340 345 4731 Val Ser Ile Leu Ala Ile Tyr Ala Gly Ala Ile Ara 355 360 4734 Pro Pro His Phe Pro Val Cys Met Leu Gly Asn Ara 375 4737 Arg His Ile Asp Val Cys Ser Lys Thr Lys Glu 395 4740 Val Pro Ser Lys Leu Trp Gly Phe Phe Cys Asn 34741 405 405 410 4743 Asn Ala Thr Cys Asp Glu Tyr Phe Val His Asn 4744 420 425 4746 Gln Gly Ile Pro Gly Leu Ala Ser Gly Ile Ile 34747 435 440 4749 Ser Asn Tyr Leu Pro Lys Gly Glu Ile Ile Glu 14750 450 455 4752 Ser Ser Asp Val Leu Gly Ser Leu Asn His Glu 3			285			
4722 Asp Asp Ala Leu Lys Glu Ser Ala Ala Met Leu 4723 305 310 315 4725 Tyr Gly Thr Ala Phe Leu Val Leu Met Val Leu 4726 325 339 4728 Val Arg Tyr Val Asn Lys Phe Ala Ser Xaa Phe 1729 340 345 4731 Val Ser Ile Leu Ala Ile Tyr Ala Gly Ala Ile 1732 355 360 4734 Pro Pro His Phe Pro Val Cys Met Leu Gly Asn 1735 370 375 4737 Arg His Ile Asp Val Cys Ser Lys Thr Lys Glu 1738 385 390 395 4740 Val Pro Ser Lys Leu Trp Gly Phe Phe Cys Asn 1741 405 405 410 4743 Asn Ala Thr Cys Asp Glu Tyr Phe Val His Asn 1744 420 425 4746 Gln Gly Ile Pro Gly Leu Ala Ser Gly Ile Ile 1747 435 435 440 4749 Ser Asn Tyr Leu Pro Lys Gly Glu Ile Ile Glu 1750 450 450 455 455 4752 Ser Ser Asp Val Leu Gly Ser Leu Asn His Glu 1750 450 450 455 455	Ala	Ala A	Ile	Phe	His	Ser
4723 305 4725 Tyr Gly Thr Ala Phe Leu Val Leu Met Val Leu Yar Val Arg Tyr Val Asn Lys Phe Ala Ser Xaa Phe Arg Tyr Val Asn Lys Phe Ala Ser Xaa Phe Arg Tyr Val Asn Lys Phe Ala Ser Xaa Phe Arg Tyr Val Asn Lys Phe Ala Ser Xaa Phe Arg Tyr Val Ser Ile Leu Ala Ile Tyr Ala Gly Ala Ile Tyr Arg Pro Pro His Phe Pro Val Cys Met Leu Gly Asn Arg Tyr Arg His Ile Asp Val Cys Ser Lys Thr Lys Glu Tyr Arg Val Pro Ser Lys Leu Trp Gly Phe Phe Cys Asn Arg Tyr Val Arg Asn Ala Thr Cys Asp Glu Tyr Phe Val His Asn Arg Tyr Arg Tyr Val Arg	300	3				
4725 Tyr Gly Thr Ala Phe Leu Val Leu Met Val Leu 4726 325 339  4728 Val Arg Tyr Val Asn Lys Phe Ala Ser Xaa Phe 174729 340 345  4731 Val Ser Ile Leu Ala Ile Tyr Ala Gly Ala Ile 174732 355 360  4734 Pro Pro His Phe Pro Val Cys Met Leu Gly Asn 17473 Arg His Ile Asp Val Cys Ser Lys Thr Lys Glu 174738 385 390 395  4740 Val Pro Ser Lys Leu Trp Gly Phe Phe Cys Asn 1741 405 410  4743 Asn Ala Thr Cys Asp Glu Tyr Phe Val His Asn 1744 420 425  4746 Gln Gly Ile Pro Gly Leu Ala Ser Gly Ile Ile 1747 435 435 440  4749 Ser Asn Tyr Leu Pro Lys Gly Glu Ile Ile Glu 1750 450 455 455  4752 Ser Ser Asp Val Leu Gly Ser Leu Asn His Glu 1750 450 455	Asn	Leu A	Asn	Met	Arg	Val
4726 325 339 4728 Val Arg Tyr Val Asn Lys Phe Ala Ser Xaa Phe 1 4729 340 345 4731 Val Ser Ile Leu Ala Ile Tyr Ala Gly Ala Ile 1 4732 355 360 4734 Pro Pro His Phe Pro Val Cys Met Leu Gly Asn 1 4735 370 375 4737 Arg His Ile Asp Val Cys Ser Lys Thr Lys Glu 1 4738 385 390 395 4740 Val Pro Ser Lys Leu Trp Gly Phe Phe Cys Asn 3 4741 405 410 4743 Asn Ala Thr Cys Asp Glu Tyr Phe Val His Asn 1 4744 420 425 4746 Gln Gly Ile Pro Gly Leu Ala Ser Gly Ile Ile 3 4747 435 440 4749 Ser Asn Tyr Leu Pro Lys Gly Glu Ile Ile Glu 1 4750 450 455 4752 Ser Ser Asp Val Leu Gly Ser Leu Asn His Glu 3		315				320
4728 Val Arg Tyr Val Asn Lys Phe Ala Ser Xaa Phe 1 4729 340 345 4731 Val Ser Ile Leu Ala Ile Tyr Ala Gly Ala Ile 1 4732 355 360 4734 Pro Pro His Phe Pro Val Cys Met Leu Gly Asn 1 4735 370 375 4737 Arg His Ile Asp Val Cys Ser Lys Thr Lys Glu 1 4738 385 390 395 4740 Val Pro Ser Lys Leu Trp Gly Phe Phe Cys Asn 3 4741 405 410 4743 Asn Ala Thr Cys Asp Glu Tyr Phe Val His Asn 1 4744 420 425 4746 Gln Gly Ile Pro Gly Leu Ala Ser Gly Ile Ile 3 4747 435 440 4749 Ser Asn Tyr Leu Pro Lys Gly Glu Ile Ile Glu 1 4750 450 455 4752 Ser Ser Asp Val Leu Gly Ser Leu Asn His Glu 3	Val	Leu 1	Val	Phe	Ile	Gly
4729 340 345 4731 Val Ser Ile Leu Ala Ile Tyr Ala Gly Ala Ile I 4732 355 360 4734 Pro Pro His Phe Pro Val Cys Met Leu Gly Asn I 4735 370 375 4737 Arg His Ile Asp Val Cys Ser Lys Thr Lys Glu I 4738 385 390 395 4740 Val Pro Ser Lys Leu Trp Gly Phe Phe Cys Asn I 4741 405 410 4743 Asn Ala Thr Cys Asp Glu Tyr Phe Val His Asn I 4744 420 425 4746 Gln Gly Ile Pro Gly Leu Ala Ser Gly Ile Ile I 4747 435 440 4749 Ser Asn Tyr Leu Pro Lys Gly Glu Ile Ile Glu I 4750 450 455 4752 Ser Ser Asp Val Leu Gly Ser Leu Asn His Glu II					335	
4731 Val Ser Ile Leu Ala Ile Tyr Ala Gly Ala Ile 14732 355 360 4734 Pro Pro His Phe Pro Val Cys Met Leu Gly Asn Ada 375 375 4737 Arg His Ile Asp Val Cys Ser Lys Thr Lys Glu 395 4740 Val Pro Ser Lys Leu Trp Gly Phe Phe Cys Asn 34741 405 410 4743 Asn Ala Thr Cys Asp Glu Tyr Phe Val His Asn Ada 420 425 4746 Gln Gly Ile Pro Gly Leu Ala Ser Gly Ile Ile 34747 435 440 4749 Ser Asn Tyr Leu Pro Lys Gly Glu Ile Ile Glu 34750 450 455 4752 Ser Ser Asp Val Leu Gly Ser Leu Asn His Glu 3	Leu .	he I	Ala	Cys	Val	Ile
4732 355 360 4734 Pro Pro His Phe Pro Val Cys Met Leu Gly Asn A 4735 370 375 4737 Arg His Ile Asp Val Cys Ser Lys Thr Lys Glu 1 4738 385 390 395 4740 Val Pro Ser Lys Leu Trp Gly Phe Phe Cys Asn 3 4741 405 410 4743 Asn Ala Thr Cys Asp Glu Tyr Phe Val His Asn A 4744 420 425 4746 Gln Gly Ile Pro Gly Leu Ala Ser Gly Ile Ile Glu 1 4747 435 440 4749 Ser Asn Tyr Leu Pro Lys Gly Glu Ile Ile Glu 1 4750 450 455 4752 Ser Ser Asp Val Leu Gly Ser Leu Asn His Glu 1				350		
4734 Pro Pro His Phe Pro Val Cys Met Leu Gly Asn A 4735 370 375 4737 Arg His Ile Asp Val Cys Ser Lys Thr Lys Glu I 4738 385 390 395 4740 Val Pro Ser Lys Leu Trp Gly Phe Phe Cys Asn 3 4741 405 410 4743 Asn Ala Thr Cys Asp Glu Tyr Phe Val His Asn A 4744 420 425 4746 Gln Gly Ile Pro Gly Leu Ala Ser Gly Ile Ile Glu I 4747 435 440 4749 Ser Asn Tyr Leu Pro Lys Gly Glu Ile Ile Glu I 4750 450 455 4752 Ser Ser Asp Val Leu Gly Ser Leu Asn His Glu I	Lys	lle I	Ser	Ser	Phe	Ala
4735 370 375 4737 Arg His Ile Asp Val Cys Ser Lys Thr Lys Glu 1 4738 385 390 395 4740 Val Pro Ser Lys Leu Trp Gly Phe Phe Cys Asn 3 4741 405 410 4743 Asn Ala Thr Cys Asp Glu Tyr Phe Val His Asn 4 4744 420 425 4746 Gln Gly Ile Pro Gly Leu Ala Ser Gly Ile Ile 3 4747 435 440 4749 Ser Asn Tyr Leu Pro Lys Gly Glu Ile Ile Glu 1 4750 450 455 4752 Ser Ser Asp Val Leu Gly Ser Leu Asn His Glu 3			365			
4737 Arg His Ile Asp Val Cys Ser Lys Thr Lys Glu 1 4738 385 390 395 4740 Val Pro Ser Lys Leu Trp Gly Phe Phe Cys Asn 3 4741 405 410 4743 Asn Ala Thr Cys Asp Glu Tyr Phe Val His Asn 4 4744 420 425 4746 Gln Gly Ile Pro Gly Leu Ala Ser Gly Ile Ile 3 4747 435 440 4749 Ser Asn Tyr Leu Pro Lys Gly Glu Ile Ile Glu 1 4750 450 455 4752 Ser Ser Asp Val Leu Gly Ser Leu Asn His Glu 3	Arg	Asn A	Thr	Leu	Ser	Ser
4738 385 4740 Val Pro Ser Lys Leu Trp Gly Phe Phe Cys Asn 34741 405 4743 Asn Ala Thr Cys Asp Glu Tyr Phe Val His Asn 44744 420 4746 Gln Gly Ile Pro Gly Leu Ala Ser Gly Ile Ile 34747 435 4749 Ser Asn Tyr Leu Pro Lys Gly Glu Ile Ile Glu 14750 450 4752 Ser Ser Asp Val Leu Gly Ser Leu Asn His Glu 3	380					
4740 Val Pro Ser Lys Leu Trp Gly Phe Phe Cys Asn 3 4741 405 410 4743 Asn Ala Thr Cys Asp Glu Tyr Phe Val His Asn 4 4744 420 425 4746 Gln Gly Ile Pro Gly Leu Ala Ser Gly Ile Ile 3 4747 435 440 4749 Ser Asn Tyr Leu Pro Lys Gly Glu Ile Ile Glu 1 4750 450 455 4752 Ser Ser Asp Val Leu Gly Ser Leu Asn His Glu 3	Ile		Asn	Asn	Met	
4741 405 410 4743 Asn Ala Thr Cys Asp Glu Tyr Phe Val His Asn A 4744 420 425 4746 Gln Gly Ile Pro Gly Leu Ala Ser Gly Ile Ile I 4747 435 440 4749 Ser Asn Tyr Leu Pro Lys Gly Glu Ile Ile Glu I 4750 450 455 4752 Ser Ser Asp Val Leu Gly Ser Leu Asn His Glu I						400
4743 Asn Ala Thr Cys Asp Glu Tyr Phe Val His Asn A 4744 420 425 4746 Gln Gly Ile Pro Gly Leu Ala Ser Gly Ile Ile 3 4747 435 440 4749 Ser Asn Tyr Leu Pro Lys Gly Glu Ile Ile Glu I 4750 450 455 4752 Ser Ser Asp Val Leu Gly Ser Leu Asn His Glu 3	Ser	Asn S	Ser	Gln		Phe
4744 420 425 4746 Gln Gly Ile Pro Gly Leu Ala Ser Gly Ile Ile 1 4747 435 440 4749 Ser Asn Tyr Leu Pro Lys Gly Glu Ile Ile Glu I 4750 450 455 4752 Ser Ser Asp Val Leu Gly Ser Leu Asn His Glu I					415	
4746 Gln Gly Ile Pro Gly Leu Ala Ser Gly Ile Ile 14747 435 440 4749 Ser Asn Tyr Leu Pro Lys Gly Glu Ile Ile Glu I4750 450 455 4752 Ser Ser Asp Val Leu Gly Ser Leu Asn His Glu I	Asn	Asn A	Val		Ser	Ile
4747 435 440 4749 Ser Asn Tyr Leu Pro Lys Gly Glu Ile Ile Glu I 4750 450 455 4752 Ser Ser Asp Val Leu Gly Ser Leu Asn His Glu I				430		
4749 Ser Asn Tyr Leu Pro Lys Gly Glu Ile Ile Glu 1 4750 450 455 4752 Ser Ser Asp Val Leu Gly Ser Leu Asn His Glu 1	Thr	le 7	Glu	Asn	Leu	Trp
4750 450 455 4752 Ser Ser Asp Val Leu Gly Ser Leu Asn His Glu			445			
4752 Ser Ser Asp Val Leu Gly Ser Leu Asn His Glu	-		Pro	Ser	Ala	Lys
	460					
4753 465 470 475	Tyr		Val	Leu	Val	
						480
4755 Ile Thr Thr Ser Phe Thr Leu Leu Val Gly Ile	Phe	le E	Phe	Pro		Val
4756 485 490					495	
4758 Thr Gly Ile Met Ala Gly Ser Asn Arg Ser Gly A	Asp	Sly A	Leu	Lys	Asp	Ala





RAW SEQUENCE LISTING DATE: 05/08/2001 PATENT APPLICATION: US/09/835,976 TIME: 15:55:17

Input Set : A:\PTO.txt

Output Set: N:\CRF3\05082001\I835976.raw

4759				500					505					510		
4761	Gln	Lys	Ser	Ile	Pro	Ile	Gly	Thr	Ile	Leu	Ala	Ile	Leu	Thr	Thr	Ser
4762			515					520					525			
4764	Phe	Val	Tyr	Leu	Ser	Asn	Val	Val	Leu	Phe	Gly	Ala	Cys	Ile	Glu	Gly
4765		530					535					540				
4767	Val	Val	Leu	Arg	Asp	Lys	Phe	Gly	Asp	Ala	Val	Lys	Gly	Asn	Leu	Val
4768	545					550					555					560
4770	Val	Gly	Thr	Leu	Ser	Trp	Pro	Ser	Pro	Trp	Val	Ile	Val	Ile	Gly	Ser
4771					565					570					575	
4773	Phe	Phe	Ser	Thr	Cys	Gly	Ala	Gly	Leu	Gln	Ser	Leu	Thr	Gly	Ala	Pro
4774				580					585					590		
4776	Arg	Leu	Leu	Gln	Ala	Ile	Ala	Lys	Asp	Asn	Ile	Ile	Pro	Phe	Leu	Arg
4777			595					600					605			
4779	Val	Phe	Gly	His	Ser	Lys	Ala	Asn	Gly	Glu	Pro	Thr	Trp	Ala	Leu	Leu
4780		610					615					620				
4782	Leu	Thr	Ala	Ala	Ile	Ala	Glu	Leu	Gly	Ile	Leu	Ile	Ala	Ser	Leu	Asp
4783						630					635				•	640
4785	Leu	Val	Ala	Pro		Leu	Ser	Met	Phe		Leu	Met	Cys	Tyr		Phe
4786					645					650					655	
4788	Val	Asn	Leu		Cys	Ala	Leu	Gln		Leu	Leu	Arg	Thr		Asn	Trp
4789				660					665					670		
4791	Arg	Pro	_	Phe	Arg	Tyr	Tyr		Trp	Ala	Leu	Ser		Met	Gly	Met
4792		_	675		_			680	_	_		_	685		_	_
4794	Ser		Cys	Leu	Ala	Leu		Phe	Ile	Ser	Ser	-	Tyr	Tyr	Ala	Ile
4795		690					695			_	_	700			_	
4797		Ala	Met	Val	Ile		Gly	Met	Ile	Tyr		Tyr	Ile	Glu	Tyr	
4798				_	~3	710		_	- 1		715			_	_	720
4800	GIA	Ala	Glu	гàг		Trp	GIY	Asp	GIA		Arg	GTA	Leu	Ser		Ser
4801	.1-	11-	<b>3</b>	nh.	725	T	T	<b>3</b>	T	730	C1	C1	D	D	735	m la
4803 4804	Ala	Ala	Arg	740	ALG	Leu	Leu	Arg	745	Gru	GIU	GTÅ	Pro	750	HIS	THE
4804	T	N co	m		Dro	Cln	T OU	T OU		Lon	LOU	Tuc	T 011		C1	Non.
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	T OU	uic		Two	uic	Dro	720		Tau	Thr-	Dho	A 1 =		Gln.	Lau	Luc
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4812	7 1 a	–	Two	C1 w	Yaa	Thr		Va 1	Clv	Sar	Va1		Va 1	C1 v	Acn	Pho
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<120> PURIFIED AND ISOLATED POTASSIUM-CHLORIDE COTRANSPORTER NUCLEIC ACIDS AND POLYPEPTIDES THERAPEUTIC AND SCREENING METHODS USING SAME

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